



## **Predicting tick abundance in Southern Scandinavia using machine learning techniques and satellite imagery – a part of the ScandTick Innovation project**

**Kjær, Lene Jung; Korslund, L.; Kjelland, V.; Slettan, A.; Andreassen, Å. K.; Paulsen, K. M.; Christensson, M.; Kjellander, P.; Teräväinen, M.; Soleng, A.**

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## Predicting tick abundance in Southern Scandinavia using machine learning techniques and satellite imagery – a part of the ScandTick Innovation project

Kjær, L. J.<sup>1</sup>, Korslund, L.<sup>2</sup>, Kjelland, V.<sup>2</sup>, Slettan, A.<sup>2</sup>, Andreassen, Å. K.<sup>3</sup>, Paulsen, K. M.<sup>3</sup>, Christensson, M.<sup>4</sup>, Kjellander, P.<sup>4</sup>, Teräväinen, M.<sup>4</sup>, Soleng, A.<sup>5</sup>, Edgar, K. S.<sup>5</sup>, Lindstedt, H. H.<sup>5</sup>, Schou, K. K.<sup>1</sup>, Bødker, R.<sup>1</sup>

<sup>1</sup>Section for Diagnostics and Scientific Advice, Technical University of Denmark, National Veterinary Institute, Copenhagen, Denmark

<sup>2</sup>Department of Natural Sciences, University of Agder, Agder, Norway

<sup>3</sup>Department of Virology, Norwegian Institute of Public health, Oslo, Norway

<sup>4</sup>Department of Ecology; Wildlife Ecology Unit, Swedish University of Agricultural Sciences, Grimsö, Sweden

<sup>5</sup>Department of Pest Control, Norwegian Institute of Public health, Oslo, Norway

In recent years, focus on tick-borne diseases has increased as diseases such as Lyme disease and tick-borne encephalitis have become more widespread and today represent a real health problem in many parts of Europe. More effective control and prevention of these diseases requires a better understanding of the factors affecting the vectors as well as pathogen survival and propagation. Hence, there is a great need for analyses and models that can clarify the main causes of changes in the transmission of disease and predict how vectors and their associated diseases are distributed now and possibly in the future.

As a part of the ScandTick Innovation project, we surveyed and collected ticks at 30+ sites in each of Denmark, southern Norway and south-eastern Sweden. We measured relative tick abundance using north- and east- facing line transect, where number of larvae, nymphs and adult females and males were counted at each 50 m transect. We used the abundance data obtained along with 37 environmental satellite images to run the Boosted Regression Tree machine learning algorithm in VecMap software to predict relative tick abundance in southern Scandinavia. The predicted abundance had a positive correlation with observed abundance and the spatial variation found corresponds well with known abundance and distributions of ticks in Scandinavia, with higher abundance in Denmark compared to Norway and Sweden. Because the abundance was strongly correlated with forested habitats the risk areas are much larger in Sweden and Norway compared to Denmark. In both the Norwegian and Swedish regions, abundance was markedly higher nearer the coastline.

Machine learning techniques allow us to predict for larger areas without having to perform extensive sampling all over the region in question. The results from these models can be used in epidemiological models and can help us determine areas under risk of disease transmission and help us interpret human incidence data. Next step will be to analyze the collected ticks for pathogens and using the same machine learning techniques to develop prevalence maps of the ScandTick region.